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[Continued on next page]

(54) Title: POLYPETIDES AND NUCLEIC ACIDS ENCODING SAME

(57) Abstract: Disclosed herein are nucleic acid sequences that encode novel polypeptides. Also disclosed are polypeptides encoded by these nucleic acid sequences, and antibodies, which immunospecifically-bind to the polypeptide, as well as derivatives, variants, mutants, or fragments of the aforementioned polypeptide, polynucleotide, or antibody. The invention further discloses therapeutic, diagnostic and research methods for diagnosis, treatment, and prevention of disorders involving any one of these novel human nucleic acids and proteins.

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(BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

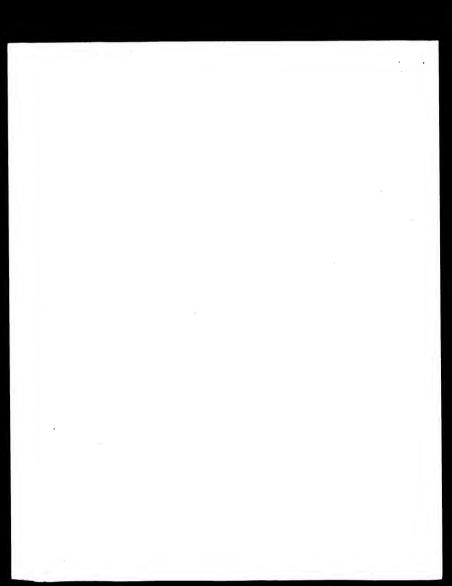
polynucleotides" and the corresponding encoded polypeptides are referred to as "NOVX polypeptides" or "NOVX proteins." Unless indicated otherwise, "NOVX" is meant to refer to any of the novel sequences disclosed herein. Table A provides a summary of the NOVX nucleic acids and their encoded polypeptides.

TABLE A. Sequences and Corresponding SEO ID Numbers

NOVX ASSIGNMENT	Internal Identification	SEQ ID NO (nucleic acid)	SEQ ID NO (polypeptide)	Homology
1	CG55758-01	1	2	SCUBE1-like
2a	CG55724-01	3	4	Adipocyte Complement Related Protein
2b	CG55724-03	5	6	Cq1 TNF-like
2c	CG55724-04	7	8	Cq1 TNF-like
2d	CG55724-06	9	10	Cq1 TNF-like
3	CG50345-01	11	12	β-Adrenergic Receptor Kinase-like
4	CG50301-01	13	14	TENM4-like
5a	CG55764-01	15	16	Out At First-like
5b	CG55764-02	17	18	Out At First-like
6a	CG55704-01	19	20	EphA6-chk-like
6ь	CG55704-03	21	22	EphA6-ehk-like
7	CG94323538	23	24	Glucose Transporter-like
8	CG95545-01	25	. 26	Type Ia Membrane Sushi- containing domain
9	CG95545-02	27	28	Type Ia Membrane Sushi- containing domain
. 10a	CG55746-01	29	30	Butyrophilin-like
10Ь	CG55746-05	31	32	Butyrophilin Precursor B7- DC
11	CG50329-01	33	34	Butyrophilin-like

NOVX nucleic acids and their encoded polypeptides are useful in a variety of applications and contexts. The various NOVX nucleic acids and polypeptides according to the invention are useful as novel members of the protein families according to the presence of domains and sequence relatedness to previously described proteins. Additionally, NOVX nucleic acids and polypeptides can also be used to identify proteins that are members of the family to which the NOVX polypeptides belong.

NOV1 is homologous to an EGF-Related SCUBB1-like family of proteins. Thus, the NOV1 nucleic acids, polypeptides, antibodies and related compounds according to the

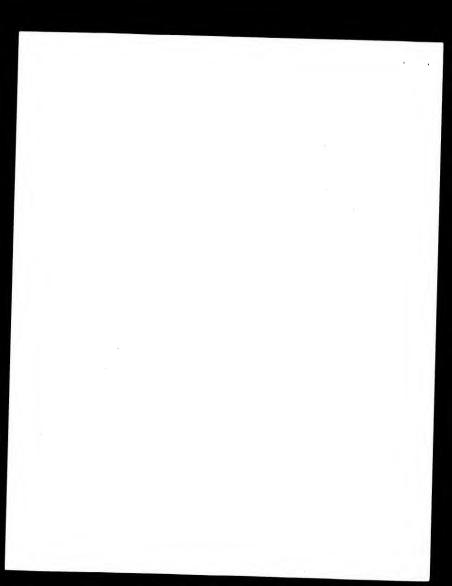


section below. The disclosed NOV3 polypeptide has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated NOV3 epitope is from about amino acids 20 to 70. In another embodiment, a contemplated NOV3 epitope is from about amino acids 95 to 115. In other specific embodiments, contemplated NOV3 epitopes are from about amino acids 120 to 190, 280 to 300, 305 to 375, 395 to 420, and 415 to 660.

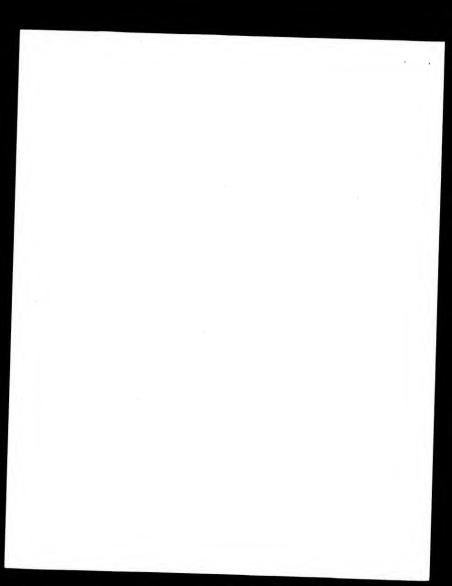
NOV4

A disclosed NOV4 nucleic acid of 8354 nucleotides is set forth as SEQ ID NO:13 (designated CuraGen Acc. No. CG50301-01) encoding a TEN-M4-like protein is shown in Table 4A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 35-37 and ending with a TAG codon at nucleotides 8342-8344. Putative untranslated regions are indicated by underline.

Table 4A.	
NOV4 Polynucleotide	
CEO ID NO.13	
A CONTRACTOR OF THE PROPERTY O	60
TTTGTGGATGTGGAGGAGGGGGGGGGGGGGGGGGGAGGGCGGTACACCAGGTCGTCGGGGACAG CGCTCGCTGACCCGGCGCGCGGACGCGGACGCCGACGCTCALCACACAGCTCGTCGAAGGCCTACGA	120
CGCTCGCTGACCCGGCGCGCGACGCGCGAGGGCCCGCTACGACGCCTACGA GAGGAGGGCAAAGCCCCGCAGAAATCGTACAGCTCCAGGAGACCCTGAAGGCCTACGA GAGGAGGGCAAAGCCCCGCAGAAATCGTACAGCTCAAGACATTGTGCCGCAGGAGGCCGA	180
GAGGAGGCAAAGCCCCGCAGAAATCGTACAGCACATTGTGCCGCAGAGGCCGA CAGGACGCCCGCCTAGCCTA	240
CAGGACGCCGCCTAGCCTATGGCAGCGCGTCAAAGGACTTGGGCTGGAAGAAGTAAC GAATTCTGCCGCACAGGTGCCAACTTCACCCTGCGGAGGCTGGGGCTAGGAGAAGTAAC	300
GAATTCTGCCGCACAGGTGCCAACTTCACCCTGCGCGAGAGCCCCAATGCGGCTACTCCAT GCCCCTCACGGGACCCTGTACCGGACAGACATTGGCCTGCCCCAATGCGGCTACTCCAT GCCCCTCACGGGACCCTGTACCGGACAGACATTGCCCTGAGCACCCCCGT	360
CCCCCTCACGGGACCCTGTACCGGACAGACATACACGGTGCTGTCCCCTGAGCACCCCGT	420
GGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGCTCCTGCCTG	480
CGTCTGTGGGCCGGAGCACACGGTCAGGGGGAAACACTGAGACTGATCATCGGGGGG TCCAATCTCACACTCACCGACACCGAGACATGAGCATGAGACTGATCATCGGGCGC TCCAATCTCACACTCACCGACACCGAGACATGAGACTCTGGCACGCCCACACCCC	540
TCCARTCTCACACTCACCGACACCGAGGATGAAACLIC TOURACTCACACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	600
CTGCAGAACCACGCGGGCTCCGGACGCCGCCGCCGCCGCCGCCGACTTCACGCCGAGGAG CAACCAGCACCACGCGGCCTCCATTAACTCCCTGAACCGGGGCAACTTCACGGCGGGGGCGCCC	660
TAACCAGCACCACGGGCCTCCATTAACTCCCTGAACCGGAGAGCCCCCTGCGGGGGGGCCCCAACCACCAGCCCCCAGGGACCACTCGCTCTCCGGAGAGCCCCCCTGCGGGGGCCCCCACGGACCACTCGCTCTCCAGAGAGCCCCCCTGGAGAC	720
AACCCCAGCCCGGCCCCCACGGACCACTCGCTCTCGAACACCCCCTGGAGAC	780
CAGGAGCCTGCCCACGCCCAGGAGAACTGGCTGCTGCTGCTCACTGAGATGGA	840
AGGAACCTAGGCAAGCAGCCATTCCTAGGGAACCTAGGCCACTTCCTCTCTCAAGCC	900
ATTCTCGGCGCCTCCCGCCATGATGGGGCTTACAGCACCTGACGCACTGACGTCCAGCAC	960
CATTCTCGGCGCCTCCCGCCATGATGGGGCTTACAGTGAGCGCCACTGACGTCCAGCAC TGGAGGCACCTCCCCGCTCTTCTGCACCRCATGACGTCACCACTGACGTCCAGCAC TGGAGGCACCTCCCCGGCCGGCCGTCTTTAA	1020
AGTGTACTCTCCTCCGCCCCGACCCCTGCCCCCCCCCCC	1080
CTCAAGAAGCCCTCCAAGTACTGTAACTGGAAGTGCCCAAGAAGTCCACCTCTTTTGGCCTAAA	1140
TCAGCCACTCTGGTCATCCTGCTGGCATACTTTGTGTGTG	1200
CTCAGCCACTCTGGTCATCCTGCTGGCATACTTTGTGGCAGGAGGAGCACAGCAGCAGCAGCAGCACTGCAGCAGCAGAGGAGGACAGAGTTATATGAGATCACGAGGAGAGACACAGCCAGC	1260
CTGGCACCTGCAGCCGATGGAGGGGCAGATGTATGAGATCACGGCGGCTTAGACACCCC TTGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGGCACTGGCTTAGAGACACC	1320
TTGGCCTGTGCCAACCGACGTCTCCCTATACCCCACTAGGGGGGGACAG TGACAGGAAAGGAA	1380
TGACAGGAAAGGCAAAGGAACCACAGAAGAAAGCCCAGTAAGATTCCTCCTGG TTTCATAGATTCTGGAGAATTGATGATGGAAGGCGAGCCTCCCAGAAGATTCAATGTGT	1440
TTTCATAGATTCTGGGGAAATTGATGTGGGAAGGGGAGCTGTGGATCTGAAATTCAATGTGTC CACTTTCTGGAGATCTCAAGTGTTCATAGACCATCCTGTGCATCTGCAAATTCAATGTGTC	1500
CACTTTCTGGAGATCTCAAGTGTTCATAGACATCTGTGAAAAGGCCTCCCTC	1560
TCTGGGAAAGGCAGCCCTGGTTGGCATTTATGGCAGAAAAAGGCCCAGGAGGCGCGGAG ACAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCCAGGAGGCGCGGAG ACAGTTTGACTTTGTGGAGCTGCTGGAAGACAGG	1620
ACAGTTTGACTTTGTGGAGCTGCTTGGATGGCAGGAGGCCCCCCCC	1680
CCTAGAGGGGACCCCGCCAGTCTCGGGGAATTGTGCCTTTTTACAATGACGGAAAGGA CTTCATCCAGTATTTGGATTCAGGAATCTGGCACTTGGCTTTTTTACAATGACGGAAAGGA	1740
CTTCATCCAGTATTTGGATTCACGAATCNGGCACTTGGCTGGATAACTGCCCCAGCAA GTCAGAAGTGGTTTCCTTTCTCACCACTGCCATTGAGTCGGTGGATAACTGCCCCCAGCAA	1800
GTCAGAAGRGTTTCCTTTCTCACCACTGCCATTGACTGCTTCCTGGGTTTCCTGGG CTGCTATGGCAATGGTGACTGCATCTCTGGGACCTGCCACTGCTTCCTGGGTTTCCTGGG CTGCTATGGCAATGGTGACTGCTTCTTTTTTTTTT	1860
CTGCTATGGCAATGGTGACTGCATCTCTGGGGACTGCCACAATGGCCAATACATGAA CCCCGACTGTGGCAGAGCCTCCTGCCCCGTGCTCTCTTAGGCGAAATGGCCAATACATGAA	1920
CCCGACTGTGGCAGAGCCTCCTGCCCCGTGCTCTTAGCGAAACGATGTGCCCACCAACCA	1980
AGGCAGATGCTTGTGCCACAGTGGCTGGAAAGGCGCTGATCACGGGCACCTGCATCTGCAA GTGTATCGATGTGGCCTGCAGCAACCATGGCACTGCATCACGGGCACCTGCATCTGCAA	2040
GTGTATCGATGTGGCCTGCAGCAACCATGGCACCACGTGGACCCCACATGTTCAGG CCCTGGCTACAAGGGCGAGAGCTGTGAGGAAGTGGACTGCATGGACCCACATGTTCAGG CCCTGGCTACAAGGGCGAGAGCTGTAGGAAGTGGACTGATTTGTAGAATTGGGAGGCACCAACTG	2100
CCCTGGCTACAAGGCCAGAAGCTGTGAGGAAGTGGAT TO CATACAGGATGCGAGGAGCACCAACTGCGGGGTGTCTGCGTGAGAGGCGAATGCCATTGCTTTGTGTGGATGGGATGCACTTCCTCCCGGA	2160
CCGGGGTGTCTGCGTGAGAGGCGAATGCCATTGCTTTTGTGCGGAACCTTCCTCCCGGA CGAGACCCCCAGGGCCACATGCTTAGACCAGTGTTCAGGCCACGGAACCTTCCTCCCGGA CGAGACCCCCAGGGCCACATGCTTAGACCAGTGTTCATAGACAGCTGTTCTATCGAGATCTG	2220
CGAGACCCCCAGGGCCACATGCTTAGACCAAGTTCTAGGCCACCTGTTCTATCGAGATCTGCACCGGGCTTTGCAGGCTGTAGACCCAAGCTGGACTGGACACGACTGTTCTATCGAGATCTG	2220



TGCTGCCGACTGTGGCCATGGCGTGTGCGTAGGGGGCACCTGCCGCTGCGAGGATGG CTGGATGGGGCAGCTGCGACCAGCGGGCCTGCCACCCGCGCTGTGCCGAGCATGGGAC 2340 CTGCCGCGACGCAAGTGCGAGTGCAGCCCTGGCTGGAATGGCGAACACTGCACCATCGC 2400 TCACTATCTGGATAGGGTAGTTAAAGAGGGTTGCCCTGGGTTGTGCAATGGCAACGGCAG 2460 ATGTACCTTAGACCTGAATGGTTGGCACTGCGTCTGCCAGCTGGACTGGAGAGGAGCTGG 2520 CTGTGACACTTCCATGGAGACTGCCTGCGGTGACAGCAAAGACAATGATGGAGATGGCCT 2580 GGTGGACTGCATGGACCCTGACTGCTGCCTCCAGCCCCTGTGCCATATCAACCCGCTGTG 2640 CCTTGGCTCCCCTRACCCTCTGGRCATCATCCAGGAGACACAGGTCCCTGTGTCACAGCA 2700 2760 AATCCCCGGGGAGAACCCCTTTGATGGAGGCATGCTTGTGTTATTCGTGGCCAAGTGAT 2820 GACATCAGATGGAACCCCCCTGGTTGGTGTGAACATCAGTTTTGTCAATAACCCTCTCTT 2880 TGGATATACAATCAGCAGGCAAGATGGCAGCTTTGACTTGGTGACAAATGGCGGCATCTC 2940 CATCATCCTGCGGTTCGAGCGGGCACCTTTCATCACACACGAGCACACCCTGTGGCTGCC 3000 ATGGGATCGCTTCTTTGTCATGGAAACCATCATCATGAGACATGAGGAGAAATGAGATTCC 3060 CAGCTGTGACCTGAGCAATTTTGCCCGCCCCAACCCAGTCGTCTCTCCATCCCCACTGAC 3120 GTCCTTCGCCAGCTCCTGTGCAGAGAAAGGCCCCATTGTGCCGGAAATTCAGGCTTTGCA 3180 GGAGGAAATCTCTATCTCTGGCTGCAAGATGAGGCTGAGCTACCTGAGCAGCCGGACCCC 3240 TGGCTACAAATCTGTCCTGAGGATCAGCCTCACCCACCCGACCATCCCCTTCAACCTCAT 3300 GAAGGTGCACCTCATGGTAGCGGTGGAGGGCCGCCTCTTCAGGAAGTGGTTCGCTGCAGC 3360 CCCAGACCTGTCCTATTATTTCATTTGGGACAAGACGAGACGTCTACAACCAGAAGGTGTT 3420 TGGGCTTTCAGAAGCCTTTGTTTCCGTGGGTTATGAATATGAATCCTGCCCAGATCTAAT 3480 CCTGTGGGAAAAAGAACAACAGTGCTGCAGGGCTATGAAATTGACGCGTCCAAGCTTGG 2540 AGGATGGAGCCTAGACATACATCATGCCCTCAACATTCAAAGTGGTATCCTGCACAAAGG 3600 GAATGGGGAGAACCAGTTTGTGTCTCAGCAGCCTCCTGTCATTGGGAGCATCATGGGCAA 3660 TGGGCGCGGAGAAGCATCTCCTGCCCCAGCTGCAACGGCCTTGCTGACGGCAACAAGCT 3720 CCTGGCCCCAGTGGCCTCACCTGTGGCTCTGACGGGAGCCTCTATGTGGGTGATTTCAA 3780 CTACATTAGAAGGATCTTCCCCTCTGGAAATGTCACCAACATCCTAGAGCTGAGGAATAA 3840 AGATTTCAGACATAGTCACAGTCCAGCACACAAATACTACCTGGCCACAGACCCCATGAG 3900 TGGGGCCGTCTTCCTTTCTGACAGCAACAGCCGGCGGGTCTTTAAAATCAAGTCCACTGT 3960 GGTGGTGAAGGACCTTGTCAAGAACTCTGAGGTGGTTGCGGGGACAGGTGACCAGTGCCT 4020 CCCTTTGATGACACTCGCTGCGGGGATGGTGGGGAAGGCCACAGAAGCCACACTCACCAA 4080 TCCCAGGGGTATTACAGTGGACAAGTTTGGGCTGATCTACTTCGTGGATGGCACCATGAT 4140 CAGACGCATCGATCAGAATGGGATCATCTCCACCCTGCTCGGCTCTAATGATCTCACATC 4200 AGCCCGGCCACTCAGCTGTGATTCTGTCATGGATATTTCCCAGGTAAGACTGGAGTGGCC 4260 CACAGACTTAGCCATCAACCCAATGGACAACTCACTTTATGTCCTCGACAACAATGTGGT 4320 CCTGCAAATCTCTGAAAACCACCAGGTGCGCATTGTCGCCGGGAGGCCCATGCACTGCCA 4380 GGTCCCTGGCATTGACCACTTCCTGCTAAGCAAGGTGGCCATCCACGCAACCCTGGAGTC 4440 AGCCACCGCTTTGGCTGTTTCACACAATGGGGTCCTGTATATTGCTGAGACTGATGAGAA 4500 AAAGATCAACCGCATCAGGCAGGTCACCACTAGTGGAGAGATCTCACTCGTTGCTGGGGC 4560 CCCCACTGGCTGTGACTGTAAAAATGATGCCAACTGTGATTGTTTTTCTGGAGACGATGG 4620 4680 GCTCTACGTGGCCGACCTTGGGAACATCCGAATTCGGTTTATCCGGAAGAACAAGCCTTT 4740 CCTCAACACCCAGAACATGTATGAGCTGTCTTCACCAATTGACCAGGAGCTCTATCTGTT 4800 TGATACCACCGGCAAGCACCTGTACACCCAAAGCCTGCCCACAGGAGACTACCTGTACAA 4860 CTTCACCTACACTGGGGACGGCGACATCACACTCATCACAGACAACAATGGCAACATGGT 4920 4 9 R O GTACTGGGTGACCATGGGCACCAACAGTGCACTCAAGAGTGTGACCACAAAGGACACGA 5040 GTTGGCCATGACATACCATGGCAATTCCGGCCTTCTGGCAACCAAAAGCAATGAAAA 5100 COGATOGACAACATTTTATGAGTACGACAGCTTTGGCCGCCTGACAAATGTGACCTTCCC 5160 TACTGGCCAGGTGAGCAGTTTCCGAAGTGATACAGACAGTTCAGTGCATGTCCAGGTAGA 5220 GACCTCCAGCAAGGATGATGTCACCATAACCACCAACCTGTCTGCCTCAGGCGCCCTTCTA 5280 CACACTGCTGCAAGACCAAGTCCGGAACAGCTACTACATCGGGGCCGATGGCTCCTTGCG 5340 5400 CACCGTCAACCCCACCGTGGGCAAGAGGAATGTCACGCTGCCCATCGACAACGGCCTCAA 5460 CCTGGTGGAGTGGCGCAGCGCAAAGAGCAGGCTCGGGGCCAGGTCACTGTCTTTGGGCG 5520 CCGGCTGCGGGTGCACAACCGAAATCTCCTATCTCTGGACTTTGATCGCGTAACACGCAC 5580 AGAGAAGATCTATGATGACCACCGCAAGTTCACCCTTCGGATTCTGTACGACCAGGCGGG 5640 GCGGCCCAGCCTCTGGTCACCCAGCAGCAGGCTGAATGGTGTCAACGTGACATACTCCCC 5700 TGGGGGTTACATTGCTGGCATCCAGAGGGGCATCATGTCTGAAAGAATGGAATACGACCA 5760 GGCGGCCGCATCACATCCAGGATCTTCGCTGATGGGAAGACATGGAGCTACACATACTT 5820 AGAGAAGTCCATGGTGCTGCTACTACACAGCCAGAGGCAGTATATCTTTGAGTTCGACAA 5880 GAATGACCGCCTCTCTTCTGTGACGATGCCCAACGTGGCGCGGCAGACACTAGAGACCAT 5940 COGCTCAGTGGGCTACTACAGAAACATCTATCAGCCCCCTGAGGGCAATGCCTCAGTCAT 6000 ACAGGACTTCACTGAGGATGGGCACCTCCTTCACACCTTCTACCTGGGCACTGGCCGCAG 6060 GGTGATATACAAGTATGGCAAACTGTCAAAGCTGGCAGAGACGCTCTATGACACCACCAA 6120 GGTCAGTTTCACCTATGACGAGACGGCAGGCATGCTGAAGACCATCAACCTACAGAATGA 6180 GGGCTTCACCTGCACCATCCGCTACCGTCAGATTGGGCCCCTGATTGACCGACAGATCTT 6240 CCGCTTCACTGAGGAAGGCATGGTCAACGCCCGTTTTGACTACAACTATGACAACAGCTT 6300



	COGGGTGACCAGCATGCAGGCTGTGATCAACGAGACCCCACTGCCCATTGATCTCTATCG	6360
	CTATGATGATGTCTCAGGCAAGACAGAGCAGTTTGGGAAGTTTGGTGTCATTTACTATGA	6420
	CATTAACCAGATCATCACCACAGCTGTCATGACCCACCAGCATTTTGATGCATATGG	6480
	CAGGATGAAGGAAGTGCAGTATGAGATCTTCCGCTCGCTC	6540
	GTATGATAACATGGGGCGAGTAGTGAAGAAGGAGCTGAAGGTAGGACCCTACGCCAATAC	6600
	CACTCGCTACTCCTATGAGTATGATGCTGACGGCCAGCTGCAGACAGTCTCCATCAATGA	6660
	CAAGCCACTCTGGCGCTACAGCTACGACCTCAATGGGAACCTGCACTTACTGAGCCCTGG	6720
	GAACAGTGCACGGCTCACACCACTACGGTATGACATCCGCGACCGCATCACTCGGCTGGG	6780
	TGACGTGCAATACAAGATGGATGAGGATGGCTTCCTGAGGCAGCGGGGGGGG	6840
	TGAGTACAACTCAGCTGGCCTGCTCATCAAGGCCTACAACCGGGCTGGCAGCTGGAGTGT	6900
	CAGGTACCGCTACGATGGCCTGGGGCGCGCGTGTCCAGCAAGAGCAGCCACCACCACCA	6960
	CCTGCAGTTCTTCTATGCAGACCTGACCAACCCCACCAAGGTCACCCACC	7020
	CTCCAGCTCTGAGATCACCTCCCTCTACTACGACTTGCAAGGACACCTCTTTGCCATGGA	7080
	GCTGAGCAGTGGTGATGAGTTTTACATAGCTTGTGACAACATCGGGACCCCTCTTGCTGT	7140
	CTTTAGTGGAACAGGTTTGATGATCAAGCAAATCCTGTACACAGCCTATGGGGAGATCTA	7200
	CATGGATACCAACCCCAACTTTCAGATCATCATAGGCTACCATGGTGGCCTCTATGATCC	7260
	ACTCACCAAGCTTGTCCACATGGGCCGGCGAGATTATGATGTGCTGGCCGGACGCTGGAC	7320
	TAGCCCAGACCACGAGCTGTGGAAGCACCTTAGTAGCAGCAACGTCATGCCTTTTAATCT	7380
	CTATATGTTCAAAAACAACACCCCATCAGCAACTCCCAGGACATCAAGTGCTTCATGAC	7440
	AGATGTTAACAGCTGGCTGCTCACCTTTGGATTCCAGCTACACAACGTGATCCCTGGTTA	7500
	TCCCAAACCAGACATGGATGCCATGGAACCCTCCTACGAGCTCATCCACACACA	7560
	AACGCAGGAGTGGGACAACAGCAAGTCTATCCTCGGGGTACAGTGTGAAGTACAGAAGCA	7620
	GCTCAAGGCCTTTGTCACCTTAGAACGGTTTGACCAGCTCTATGGCTCCACAATCACCAG	7680
	CTGCCAGCAGGCTCCAAAGACCAAGAAGTTTGCATCCAGCGGCTCAGTCTTTGGCAAGGG	7740
ì	GGTCAAGTTTGCCTTGAAGGATGGCCGAGTGACCACAGACATCATCAGTGTGGCCAATGA	7800
	GGATGGGCGAAGGGTTGCTGCCATCITGAACCATGCCCACTACCTAGAGAACCTGCACTT	7860
	CACCATTGATGGGGTGGATACCCATTACTTTGTGAAACCAGGACCTTCAGAAGGTGACCT	7920
	GGCCATCCTGGGCCTCAGTGGGGGGGGGGGGAACCCTGGAGAATGGGGTCAACGTCACTGT	7980
	GICCCAGATCAACACAGTACTTAATGGCAGGACTAGACGCTACACAGACATCCAGCTCCA	8040
ì	GTACGGGGCACTGTGCTTGAACACACGCTACGGGACAACGTTGGATGAGGAGAAGGCACG	8100
ì	GGTCTGGAGCTGGCCGGCAGAGAGCCGTGCGCCAAGCGTGGGCCCGCGAGCAGCAGAG	8160
	ACTGCGGGAAGGGGAAGGCCTGCGGGCCTGGACAGAGGGGGGAGAAGCAGCAGGTGCT	8220
į	GAGCACAGGGCGGGTGCAAGGCTACGACGGCTTTTTCGTGATCTCTGTCGAGCAGTACCC	8280
	AGAACTGTCAGACAGCGCCAACAACATCCACTTCATGAGACAGAGCGAGATGGGCCGGAG	8340
į	GTGACAGAGGGC	
i		

A disclosed NOV4 nucleic acid maps to chromosome 11, and is found in at least brain, spinal chord, testis, heart, lung, parathyroid, stomach, breast, colon, epidermis, ovary and kidney. A NOV4 nucleic acid has 7504 of 8359 bases (89%) identical to a gb:GENBANK-ID:AB025413|acc: AB025413.1 mRNA from Mus musculus TEN-M4.

A NOV4 polypeptide (SEQ ID NO:14) encoded by SEQ ID NO:13 is 2769 amino acid residues and is presented using the one letter code in Table 4B. Signal P, Psort and/or Hydropathy results predict that NOV4 does not have a signal peptide and is likely to be localized mitochondrial inner membrane with a certainty of 0.8363. In other embodiments, NOV4 may also be localized to the plasma membrane with a certainty of 0.65 or to the nucleus with a certainty of 0.6936.

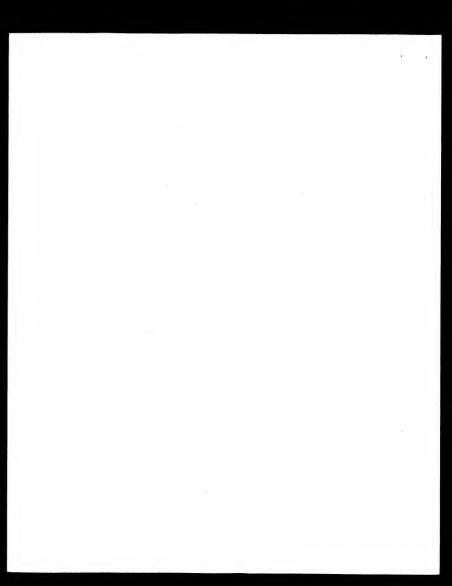


Table 4B. NOV4 Polypeptide SEO ID NO:14

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TIDNIGNNYAVRROBTIGNELALWYPDGGYWWYTKSTINSALKSYTTYGGHELAMMYTHSISS 1680 LIATKENBURGHTYFYKUDGFRUINVTFFTGGYSSFFEDTDSSYTYGGHELAMMYTHSISS 1740 NLSASGAPYTLLODGWESTYTGNDSELLLAMGEWALGTEPHLLAGTWPTVGKRWY 1800 NLSASGAPYTLLODGWESTYTGNDSELLLAMGEWALGTEPHLLAGTWPTVGKRWY 1800 RILIYDDGABPELAGTWFTGTFTGOTHGWTWARGTHTTRIKTYBERCY 1800 RILIYDDGABPELAGTWFTGTFTGOTHGWTWARGTHTTRIKTYBERCY 1800 RILIYDDGABPELAGTWFTGTGGWTWARGTHTLSWGYTRHTWO 1800 RILIYDHAGRAFTTRIKTGGEWTWARGTHTLSWGYTRHTWO 1800 REGENSKYLGOPHEGGLAHFTTGGGWTWARGTHTLSWGYTRHTWO 1800 LICTHLGBBGPCTTRYDGIGPLURGFTFFTGGWWARGTWTNDNSFRYTSMGAVINE 2100 RILIYDHAGRAFTTRYDGIGPLURGFTFFTGGWWARGTWTNDNSFRYTSMGAVINE 2100 RILIYDHAGRAFTTRYDGIGPLURGFTFFTGGWWARGTWTNDNSFRYTSMGAVINE 2100 RILILISGNSGRAFTLFTRITGTGWTTTRYSKYTDADGGGFTFTMSMGALIKA 2280 RIMHLISGNSGRAFTLFTRITGTGWTTTRYSKYTDADGGGFTFTMSMGALIKA 2280 RIMHLISGNSGREFTLAGTGTTAFTGGTGATHTTRYSKYTDADGGFTFTMSMGALIKA 2280 RIMHLISGNSGREFTLAGTGTTAFTAFTGTGATHTRICHTRYTKYTTHENHERSELTTSLYTD 2400 RICHGGTGATGTGTTAFTGTGTTAFTGTGTGATHTGTTTTTTTTTT	RFIRKNKPFINTONMYELSSPIDOKLYLFDTTGKHLYTQSLPTGDYLYNFTYTGDGDITL	1620
LIATESININGKTTFYENDSFERLINVTEPTOGVSSPREJITOSSVINOVETSSKIDDYTITT 1740 LIAGNSGAPYTHJODOVENSTYLGAGOSIELLIANGKEVALIATEVSTVOYGKNV 1800 LIPIDIGLINUSHRORKEGARGOVTVPGRELEVSINNILLISLDDDEVTETEKTYDDREKTY 1800 LIPIDIGLINUSHRORKEGARGOVTVPGRELEVSINNILLISLDDDEVTETEKTYTDREKTET 1800 LIPIDIGLINUSHRORKEGARGOVTVPGRELEVSINNILLISLDDDEVTETEKTYTDDREKTET 1800 LIKTINLOGAGIPSLAGSDSSLEGGAVIVTSPGGTALGTGGREGARGEVTOGAGGITESTREN 1800 LIKTINLOGAGIPSLAGSDSSLEGGAVTFTGGTREKTYKTGKSTGATUTTKVSSTTDDTAGAG 1800 LIKTINLOGBEPTCTTRYBGIGFHJUNGLIFFTEKSGNVARARDVNITDRSFRUTSKGAVINE 1800 LIKTINLOGAGIPSTAGGARGATER 1800 LI	TTDNNGNMVNVRRDSTGMPLWLVVPDGOVYWVTMGTNSALKSVTTQGHELAMMTYHGNSG	1680
NLEASGAPYTLIQGOVENSTYTGADGELELLIANGGEVALCTEPEILLAGTVEPTVGKRWY 1806 ILP DINGELNIVENGRREGARGAVOVTVØRELKUSHNINLIGLDDFUVTTEKTK YDDREKYT 1866 ILRILYDOAGRPSLAG PSSELAGUNVYS FOGY ILAG QUKSTUSHNINLIGHDFUVTTEKTKY TEDREKYT 1926 ILRILYDOAGRPSLAG PSSELAGUNVYS FOGY ILAG QUKSTUSHSRREGUOAGRITESITRAD 1926 ILRILYDOAGRPSLAG PSSELAGUNVYS FOGY ILAG QUKSTUSHSRREGUOAGRITESITRAD 1926 ILRILYDOAGRPSLAG AND	I LATKSNENGWTTFYEYDSFGRLTNVTFPTGOVSSFRSDTDSSVHVQVETSSKDDVTITT	1740
TLP ITENGINIVENRORREGOARGOVTVPERELEVENRINLISLDDTDEVITTERIYTDEREKTT 1860 RILTIDOAGREPSLAG SPESILGONIVETSEGGT LAGI GREMENSREWETDAGAGETISEIPAD 1920 RICHESTTILERSHWILLHEGGGVITERFURDELESVTHENNARGTLEFTERSWYTYRITYQ 1980 RICHESTTILERSHWILLHEGGGVITERFURDELESVTHENNARGTLEFTERSWYTYRITYQ 1980 RICHESTRICHGEGPTCTTERTGEREVITERGREWITERGEREVITERTHETHERGERYTYRITYG 2040 LIKTINLIGHEGPTCTTERTGIGFPLIDEQIFFFTERSHWIARGPDNITDSFRYTSHQAVINE 2120 RICHIBLINGHEGPTCTTERTGIGFPLIDEQIFFFTERSHWIARGPDNITDSFRYTSHQAVINE 2120 RICHIBLINGHEGPTCTTERTGIGFPLIDEQIFFFTERSHWIARGPDNITDSFRYTSHQAVINE 2120 RICHIBLINGHEGPTCTTERTGIGFPLIDEQIFFFTERSHWIARGPDNITDSFRYTSHQAVINE 2120 RICHIBLINGHEGPTCTTERTGIGFPLIDEQIFFTERSHWIARGPDNITDSFRYTSHQAVINE 2120 RICHIBLINGHEGPTCTTERTGIGFPLIDEQIFFTERSHWIARGPDNITGSFRYTSHQAVINE 2120 RICHIBLINGHEGPTCTTERTGIGFPLIDEQIFFTERSHWIARGPDNITGSFRYTSHQAVINE 2120 RICHIBLINGHEGPTCTTERTGIGFPLIDEQIFFTERSHWIARGPDNITGSFTTSHTD 2120 RICHIBLINGHEGPTCTTERTGIGFPLIDEQIFFTERSHWIARGPTSHTATTHOLDEGTTSHTAT	NI_SASGAPYTT.I.ODOVRNSYYI.GADGSLRIJJ.ANGMEVALQTEPHJ.LAGTVNPTVGKRNV	
LRILIYONGGEPSIANSPSSELNGWNYTYSPGGYIAGIQRGIMSERGEYDAGGEITENIPAD 1920 SEKMENTYTIGNEGWULLIGEGGGYI FEPFORMELESVYTHENVARGUITENITENGYTYPRITO 1980 PREMANSYI ODPYREDGILLHEFYIGTGERKYI TKYGELGKILAETLITDITKYSPTIDETAGG 200 SEKMENTYTONICHTI TREZGIGERUNDOT PED UTTAVARITENITENITYPRITORIAETLITAETL	TI.PIDNGI.NI.VEWRORKEOARGOVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKFT	
1980 PERENSYL DEPRENGALIFIE PROFITE PER TRUBLES YTHEN VARQITLET LES VGYYRNIYQ 2040 PERENSYL OF PHEGIGHLET PLIGTERKUT IXTGUISLE ALE TLOTT TUNNET PLIE TARM 2040 LKTINLOMEGPTCTI RYRGIGPLIORQI PEPTESGHWIAR RED WYNDNSTRUTS QQUYTE PLOE LICHT PLOE PLOE PLOE PLOE PLOE PLOE PLOE PLOE	LRILYDOAGRPSLWSPSSRLNGVNVTYSPGGYIAGIQRGIMSERMEYDQAGRITSRIFAD	
PREGNASVIQDPYENGGILHIFYIGTGRKVITKTGKLSKLAETLIDTITKVSFTTDETAGM LIKTINLQMSEGFTTTRKRQIGHGLIDQUFFFFESSMVARAPDVINNDSFKVITSMAVINE 2100 1210 1210 1210 1210 1210 1210 121	GKTWSYTYLEKSMVLLLHSOROYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYYRNIYQ	
LICTINLONGERPTCTITRIRGIGHLIDROLIFEFTERSEMVARREPUNTONSPERVISMOAVINE 21.60 EIGH IDLINENDUSSKITEGREKSENTYTINDIGH LITTAMWITHERHEPATSEMERSVYSENDAVIER 21.60 EIMPERTTONISMERVUKTELKUGETANTTRISSETDADGOLG/TYSINKEPLANKESTULA 2220 EIMPERTTONISMERVUKTELKUGETANTTRISSETDADGOLG/TYSINKEPLANKESTULA 2220 EIMPERTSONISMERVEKTERUSENTRIGUTEVARDENDERGERGEN FERRENBELLIKA 2230 EIMPERTSONISMERTERUSENTRIGUTEVARDENDERGERGEN FERRENBELLIKA 2240 EIMPERTSONISMERTERUSENTRIGUTEVARDENDERGEN FERRENBERGEN TANDEN 2340 EIMPERTSONISMERTERUSENTRIGUTEVARDENDERGEN FERRENBERGEN 2440 EIMPERTSONISMERTERUSENTRIGUTEVARDENDERGEN FERRENBERGEN 2450 EIMPERTSONISMERTERUSENTRIGUTEVARDENDERGEN FERRENBERGEN 2450 EIMPERTSONISMERTERUSENTRIGUTEVARDENDERGEN FERRENBERGEN 2450 EIMPERTSONISMERTERUSENTRIGUTEVARDENDERGEN FERRENBERGEN 2450 EIMPERTSONISMERTSONISMERTERUSENTRIGUTEVARDENBERGEN 2450 EIMPERTSONISMERTSONISMERTSONISMERTERUSENTRIGUTEVARDENBERGEN 2450 EIMPERTSONISMER	PPEGNASVIODFTEDGHLLHTFYLGTGRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGM	
PEDEIDLINKYDDVSGKTREGPEKREGVIYTDINQIITTAVMITHTHHFDÄYERMKENQYEIFR 216.6 EMMUNTOYDONKREVNERIKANGPINTRYNSYEITDAOGLOTYSINDEVBINSYIDIN 222.0 EMMILLISPONSARLIPIERDIEDRITHLEDWQYMODEOGHARGROGDIFFYNBAGILIKA 228.0 EMMILLISPONSARLIPIERDIEDRITHLEDWQYMODEOGHARGROGDIFFYNBAGILIKA 228.0 EMMILLISPONSARLIPIERDIEDRITHLEDWQYMODEOGHARGROGDIFFYNBAGILIKA 228.0 EMMILLISPONSARLIPIERDIEDHTHLEDWQYMODEOGHARGROGDIFFYNBAGILIKA 228.0 EMMILLISPONSARLIPIERDIEDHTHLEDWQYMODEOGHARGROGDIFTAYBAGILIKAN 240.0 EMMILLISPONSARLIPIERDIEDHTHLEMHISSSYNBYPENLYMPKNBUPIST 250.0 EMMILLISPONSARLIPIERDIEDHTHLEMHISSSYNBYPENLYMPKNBUPIST 250.0 EMMILLISPONSARLIPIERDIEDHTHLEMHISSSYNBYPENLYMPKNBUPIST 250.0 EMMILLISPONSARLIPIERDIEDHTHLEMHISSTYNBYPKNBUPIST 250.0 EMMUNICATION FYLLENDRIEDHTHLEMHISTIDHTHLEMHISSTYNBUPIST 250.0 EMMONIYATION FYLLENDRIEDHTHLEMHISTIDHTHTHLEMHISTIDHTHLEMHISTIDHTHLEMHISTIDHTHLEMHISTIDHTHLEMHISTIDHTHTHLEMHISTIDHTHLEMHISTIDHTHLEMHISTIDHTHLEMHISTIDHTHLEMHISTIDHTHLEMHISTIDHTHLEMH	LKTINLONEGFTCTIRYROIGPLIDROIFRFTEEGMVNARFDYNYDNSFRVTSMQAVINE	
SIAMYMNTYOYDMAGRUVKKELKUGEYANTTRYSYETDADOGLOTYSINDKPUMKYSYDLAN 2220 RINGHLIS-GRARALPIERIDE LEGELTIKLIGUVGYNDGEOGELGROGGI FETNERAGULIKA 2280 RNRAGSHEVKYRYDGLORRVSSKSSHSHEHLOFFYADLYNDFYKVTHLYNHUSSELTELYYD 2340 STREGLYDPLITEGUPHAGEDDTULAGUNTHIK (DILITAK TIGELT PEDURNFULTI 240 STREGLYDPLITEGUPHAGEDDTULAGUNTSFEREGUNGER GEYELLTYCHTONHORRESTL 250 STREGLYDPLITEGUPHAGEDDTULAGUNTSFEREGUNGER GYPELLTYCHTONHORRESTL 250 DILISVANDEGORVAN LIBRANTURNLIFTIDOVDTHYPVROPEDSCULALUGLGGGRT 2610 DILISVANDEGORVAN LIBRANTURNLIFTIDOVDTHYPVROPEDSCULALUGLGGGRT 262 2630 2630 2630 2630 2630 2630 2630	TPLPIDLYRYDDVSGKTBOFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYBIFR	
INRAGSWSVRYRYDGLORRVSSKSSHSHLQPFYADLTMPTKVTLLVMHSSSELTSLYYD AGGILFAMELSSGOEPTALOWIGTPLAVPSGTGIAHKQILTYAYGBITMDTMPTQIII 2400 3416GLYDPLTKKVBMGREDDTDLAGSWTSEDHBLWRTHSSSVMPPHLDMPRENDRFISN 2500IKCFHTDVASMLLTPGFQLANVIROPFKFDMDAMEPSVELIHTOMTOBMISHSBIJ 2520 370CEVQDQLKAPVTLERVDLAGSTTISSQDASTKKFASSGSVFVGRVYFRALDGSKVT DIIISVANEGGRRVAAILHHAHTLENLHFTIDGVDTHYVKPGPGSDLALIGLSGGRRT 2520 2520 2520 2520 2520 2520 2520 252	SLMYWMTVQYDNMGRVVKKBLKVGPYANTTRYSYBYDADGQLQTVSINDKPLWRYSYDLN	
NMAGANGWUKTYKYDOLGRRVSSKSSHSHHIGFFYADLINFYKVTLLYNHUSSELTSLYTD 2340 GEGLEANHISSGOEFFILAND GTFLAVPSSTOTHIKGULTYATGELTWINFINTIL 1340 THIGGI-MPOLTKUPMAGROUDULAGUNTSEDHHUNKULTYATGELTWINFINTIL 1340 COLKCEPTIOVSHMLIT GEGUNTVICHTEN GEGUNT 1350 THIGGI-MPOLTKUPMAGROUDULAGUNTSEDHHUNKILSSNVAPPHLYMFARNEFISM 1450 COLKCEPTIOVSHMLIT GEGUNTVICHTEN GEGUNTVICHTEN GEGUNT 1450 THIGHT GEGUNTVICHTEN GEGUNTVICHTEN GEGUNTVICHTEN GEGUNTVICHT 1550 THIGHT GEGUNTVICHTEN GEGUNTVICHTEN GEGUNTVICHTEN GEGUNTVICHT 1560 THIGHT GEGUNTVICHTEN GEGUNTVICHT GEGUNTVICHTEN GEGUNTVICHT GEGUNT	GNLHILSPGNSARLTPLRYDIEDRITRLGDVQYKMDEDGFLRQRGGDIFEYNSAGLLIKA	
STREGLYDPLITKIVEMCERDYDVLAGENTSPDHELWKHLSSSNVMEPHLYMFKNENETSD 2460 SODIKCHTIVUSMITTPGFGLANNI POTFREDMOMEPSTELLITUNKTQENDRISSIL 2520 YOCEVOGQUAPVLERPOLIGSTITSCQAB KTKKFASSSSYFCKGYKFALKGEKYT 2580 DDIISYANEGGRAVAA LIMHAHYLEKHLHFIDGVDTHYPKPGPGSGDLALIGLSGGRAT 2640 ESKYNNYTVSGNYTVLINGKTRETYDIGGVGRALLIKTRYGTINGSKRAVLELARGRAYK 2700	YNRAGSWSVRYRYDGLGRRVSSKSSHSHHLQFFYADLTNPTKVTHLYNHSSSEITSLYYD	
SOLIKCPHTUVESHLLTPGFOLENTI POTFRFDMDAMEPSYELITTOMTOSMONERSIL 2520 YOCEWIGGILGAPVILENDIGIGSTITSCOGAPKTKAPASSOSYFGKEVPEALKOGSTVT 2580 DDIISVANEGGRIVALIENDIGISTITSCOGAPKTKAPASSOSYFGKEVPEALKOGSTVT 2640 DDIISVANEGGRIVALIENDIGISTITSCOGAPKTKAPASSOSYFGKEVPEALKOGSTVT 2640 ESENGVANYIVSCINTVILKGETRETYDIOLOGYGALLGITEKTOTTIDEKRAKUFLLERARGEVER 2700	LOGHLFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNFNFQIII	
JYQCEYQKQLKAFYTIARFYQLIGSTITSCQQAFKTKFASSGSYFGKGYKFALKOGRYT DIISVANEDGRRVAAILMRAHILEMLHFITDGYDTHYFYKFGEDEGLLAILLIGSGRRT 2640 LENGYNYTYSQINTYLINGFREYFYTOIGQFGALCLINTRYGTTLDESKARVLELARGAVR 700	GYHGGLYDPLTKLVHMGRRDYDVLAGRWTSPDHBLWKHLSSSNVMPFNLYMFKNNNPISN	
IDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPDEGDLAILGLSGGRRT 2640 LENGVNVTVSQINTVLNGRTRRYTDIQLQYGALGLNTRYGTTLDEEKARVLELARQRAVR 2700	SQDIKCFMTDVNSWLLTFGFQLHNVIPGYPKPDMDAMEPSYELIHTQMKTQEWDNSKSIL	
LENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQRAVR 2700	GVQCEVQKQLKAFVTLERFDQLYGSTITSCQQAPKTKKFASSGSVFGKGVKFALKDGRVT	
LENGVMVTVSQINTVLNGRTRRYTDIQLQYGALCLMTRYGTTLDEEKARVLELARQRAVR 2700 QAWAREQQRLREGEEGLRAWTEGEKQQVLSTGRVQGYDGFFV1EVEGYPELSDSANNIEF 2760	TDIISVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGDLAILGLSGGRRT	
QAWAREQQRLREGEEGLRAWIEGEKQQVLSTGRVQGYDGFFVISVEQYPELSDSANNIHF 2760	LENGVNVTVSQINTVLNGRTRRYTDIQLQYGALCLNTRYGTTLDEEKARVLELARQRAVR	
	QAWAREQQRLREGEEGLRAWIEGEKQQVLSTGRVQGYDGFFVLEVEQYPELSDSANNIHF	2760
RQSEMGRR	MRQSEMGRR	

The full amino acid sequence of the protein of the invention was found to have 2688 of 2771 amino acid residues (97%) identical to, and 2728 of 2771 amino acid residues (98%) similar to, the 2771 amino acid residue ptnr:SPTREMBL-ACC:Q9WTS7 protein from Mus musculus TEN-M4.

NOV4 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 4C.

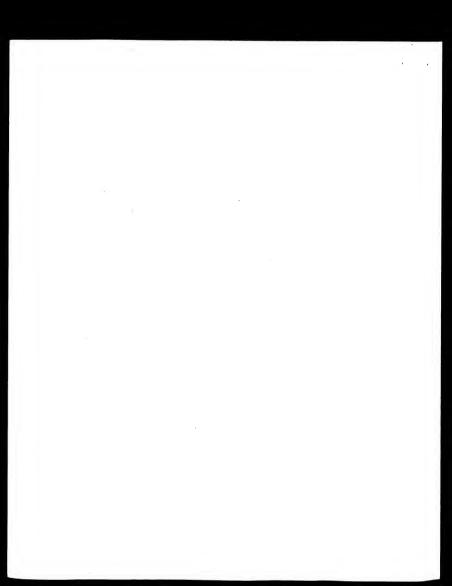


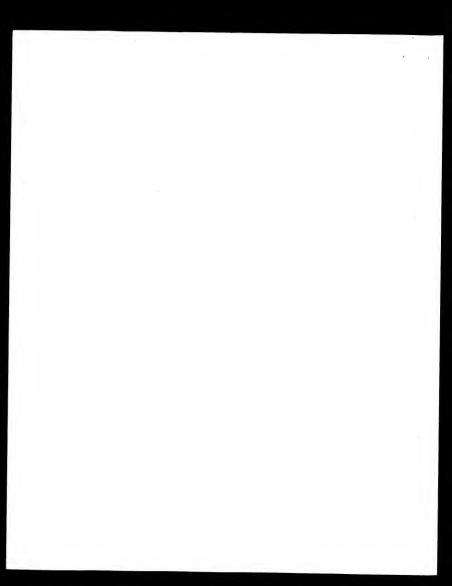
	Table 4C. BLA	ST result			,
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 16551957 dbj BAB 71206.1 (AK056531)	unnamed protein product [Homo sapiens]	730	99	99	0.0
gi 7657417 ref NP 035987.2 (NM_011857)	odd Oz/ten-m homolog 3 (Drosophila); odd Oz/ten-m homolog 1 (Drosophila) [Mus musculus]	2715	66	79	0.0
gi 13649010 ref X P_010128.3 XM_010128	odz (odd Oz/ten- m, Drosophila) homolog 1 [Homo sapiens]	2725	62	76	0.0
gi 1079143 pir S 47008	tenascin-like protein - fruit fly (Drosophila melanogaster)	2515	33	53	0.0
gi 8922444 ref NP 060574.1 (NM_018104)	hypothetical protein FLJ10474; hypothetical protein FLJ10886 [Homo sapiens]	1045	99	99	0.0

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 4D.

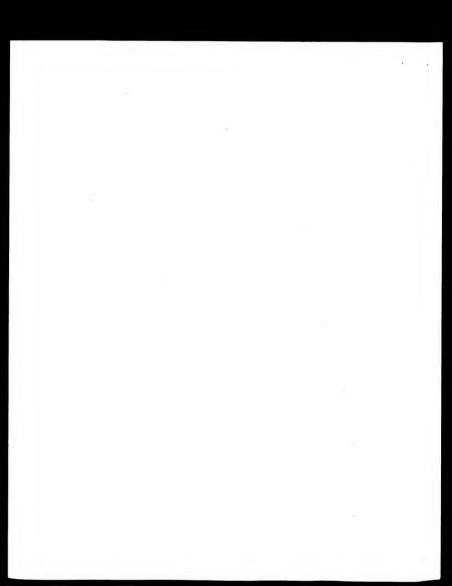
Table 4D ClustalW Analysis of NOV4

Tables 4E lists the domain description from DOMAIN analysis results against NOV4. This indicates that the NOV4 sequence has properties similar to those of other proteins known to contain this domain.

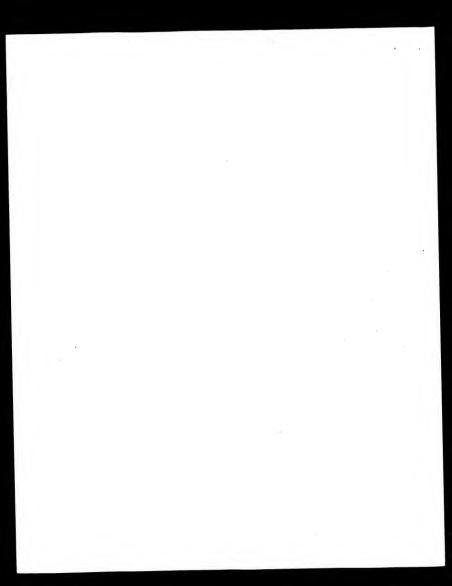
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1) MOV4 (SEQ ID NO.1.3)
2) gi[1657147 (SEQ ID NO.50)
3) gi[7657417 (SEQ ID NO.51)
4) gi[13649010 (SEQ ID NO.53)
5) gi[2079143 (SEQ ID NO.53)
6) gi[822444 (SEQ ID NO.54)
10 20 30 40 50
100744 MOVEMENTENSIT-EREDBERTISSEADSHEGKAP-QKSYSSSHTLKAP
4]136551957
gi[17657417] MOVEMENTYCOLIKEREREGERTISSEADSHEGKAP-QKSYSSSHTLKAP
4]136549010 MOQTOCKLYTGELEREREGERTISSEADSHEGKAP-QKSYSSSHTLKAP
1]13649010 MOQTOCKLYTGELEREREGERTISSEADSHEGKAP-QKSYSSSHTLKAP
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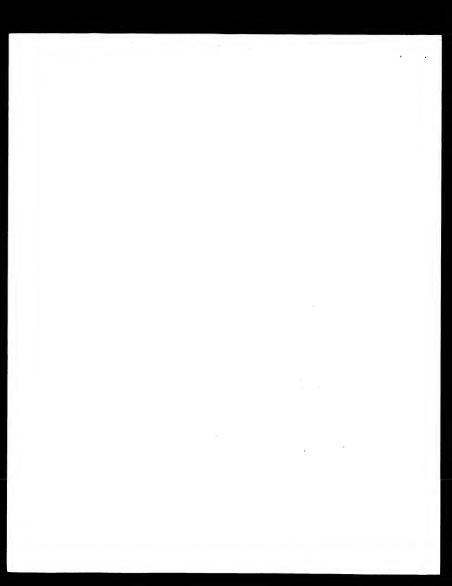
gi 1079143	
gi 8922444	
	50 70 80 90 100
	60 70 80 90 100
NOV4	DQD-ARLAYGSRVKDIVPQEARBFCRTGANFTIRESGLEEVTPPHGTLYR
NOV4 gi 16551957	DQD-ARLAIGSRVKDI VPQBABBFCKIGAUS LIREAGUEBA IFFIIO2224
gi 7657417	DHDYSKLLYGNRVKDLVHREADBYTRQGQNFTLRQ\(\)GVC\(\)SATRRGVAFC
gi 13649010	NOELRMN-YNSQSRKRKEVEKSTQEMEFCETSHTLCSGYQ
gi 13843010 gi 1079143	
gi 8922444	M. D.
52/0322444	
	110 120 130 140 150
NOV4	TDGG-GPQCGYSGGAGSDADMRADIVLGPRHPVRGWGRSTRGGRSGCLGG
gi 16551957	
gi 7657417	ABIG-TPHRGYSTSAGSDADTENBAVNSPEHANDENGRGVKSGRESCLES
gi 13649010	TDHHSUSRHGYOMENGSDVDTRTEGAASPDHALRIMIRGNKSEHESCLES
gi 1079143	PGGGGESATSVEEANTTITILIALLAAN OS BECGGESATA SEG
gi 8922444	
	160 170 180 190 200
NOV4	RANGSULTLYDERHENTETCHPGGLQN
gi 16551957 gi 7657417	RSWSAL/IIL/ID#RHENRSDSBSEQPSN
gi 13649010	RAMSALSITD#DHERKSDGENGFKFSPVCCDMEAQAGSTQDVQSSPHINQF
gi 13649010 gi 1079143	NTILSKIHNSÖVRAKNGQGIGLAQG
gi 8922444	HTHIOATINIOATTO
3-1	
	210 220 230 240 250
NOV4	HARLRTPPPPLSHAHTPNCHHAASINGLMRGNFTPRSMPSPFPTCHSLEG
gi 16551957	
gi 7657417	NPGQPTLQPLPPSHKQHPAQHHPSITGLMKNSLTNRRNQ\(\frac{1}{2}\)PPAALIP\(\frac{1}{2}\)B
gi 13649010	TERPLEPPPPPPPHACTCARKPPPAALELQRRSMTTKSQPSPAAPPTST
gi 1079143	QSGLGAAGVGSGSGSAATVTTATSA <mark>G</mark> GTAQGTQSTSASÄR <mark>A</mark> TSSAATÄS
gi 8922444	
	260 270 280 290 300
NOV4	EPPAGGAQEPAHAQENWILINSHIPLETRNIGKQPPIGTIQDNLIEMDILG
gi 16551957	BI I NOON CONTRACTOR OF THE PROPERTY OF THE PR
gi[7657417]	LQTTPESVQLQDSWVLGSHVPLESR
gi 13649010	QDSVHLHNSWVLMSNI PLETR
gi 1079143	808
gi 8922444	
	310 320 330 340 350
NOV4	asrhdgaysdghflfkpggtsplfctigpgypltsstvygpppdpldreg
gi 16551957	
	55



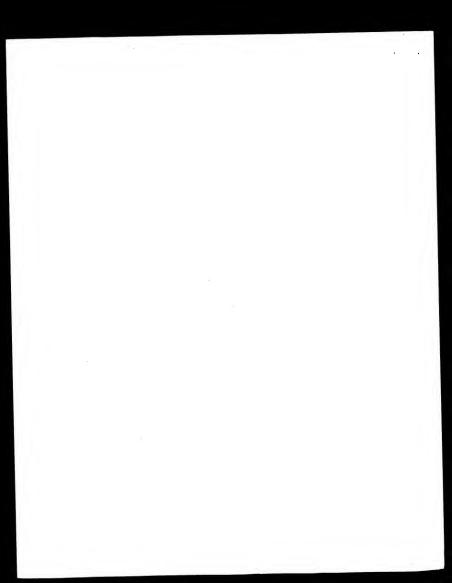
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gi 1364901	OHFLFKHGSGSSAIFSAAGONYPLITSHTVYGPPFGPLGRSG
gi 1079143	
gi 8922444	and the opposite the state of t
	360 370 380 390 400
NOV4	FARPAPHLKKPSKYCNWKCAALSAIVISATLVILLAYFVAMHLPGLNWHL
gi 16551957	
gi 7657417	LSRSAFKFKKSSKYCSWRCTALCAVGVSVLLAILLSYFIAMHLFGLNWHL
gi 13649010	FSRPAFTFNKPYRCCNWKCTALSATAITVTLALLLAYVIAVHLFGLTWQL
gi 1079143	FP
g1 8922444	
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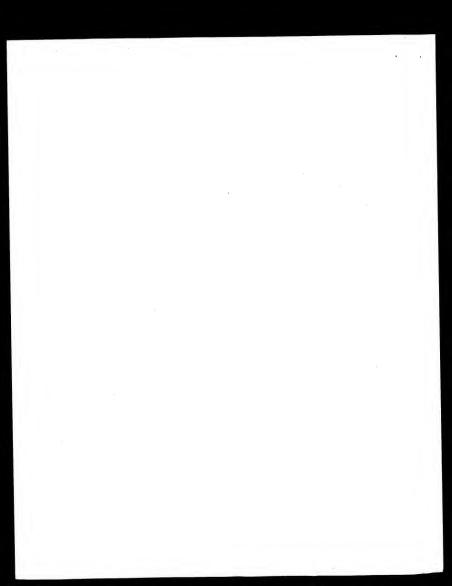
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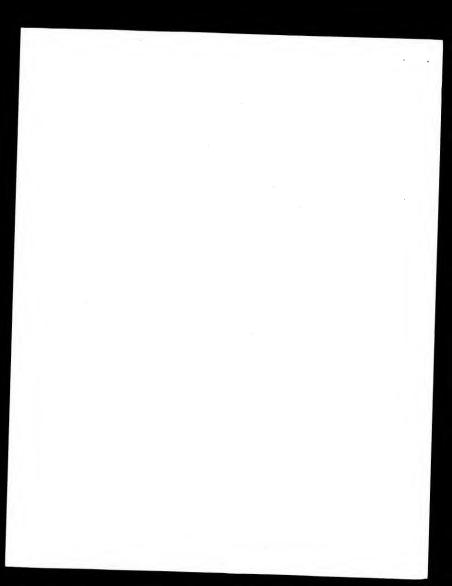
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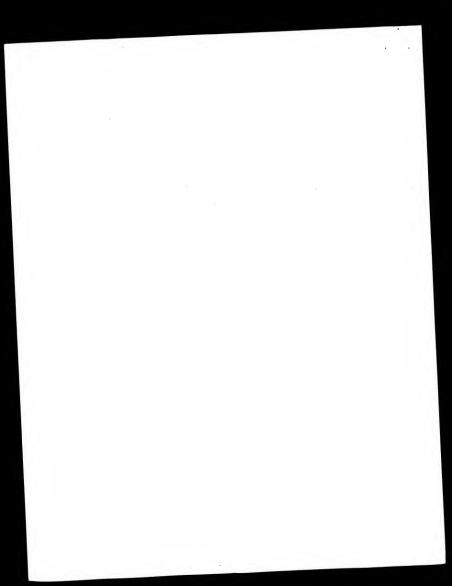
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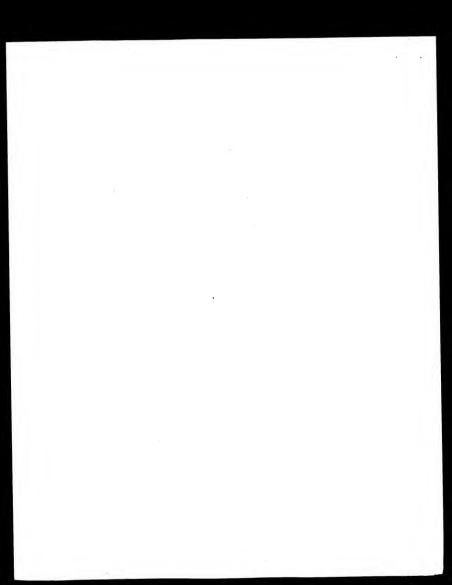
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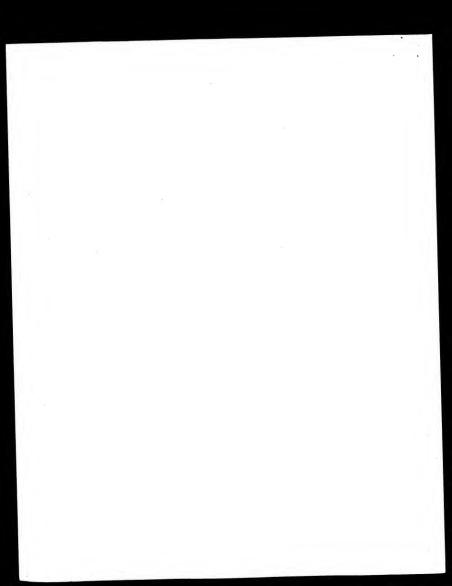
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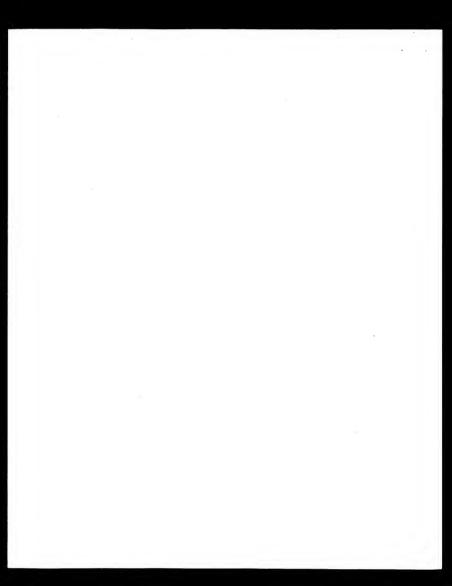


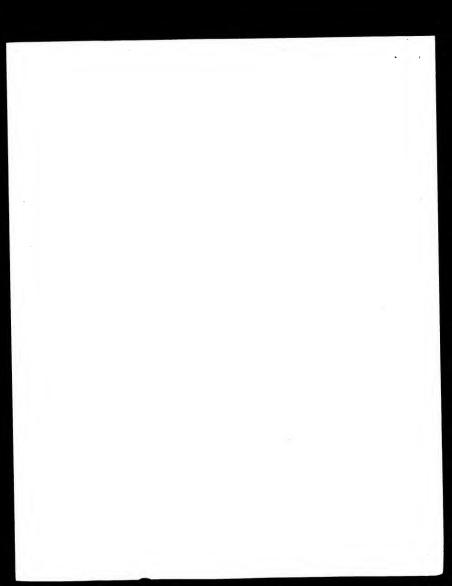
Table 4E. Domain Analysis of NOV4

gnllPfamlpfam01500, Keratin_B2, Keratin, high sulfur B2 protein. High sulfur proteins are cysteine-rich proteins synthesized during the differentiation of hair matrix cells, and form hair fibers in association with hair keratin intermediate filaments. This family has been divided up into four regions, with the second region containing 8 copies of a short repeat. This family is also known as B2 or KAP1.

CD-Length = 144 residues, 87.5% aligned

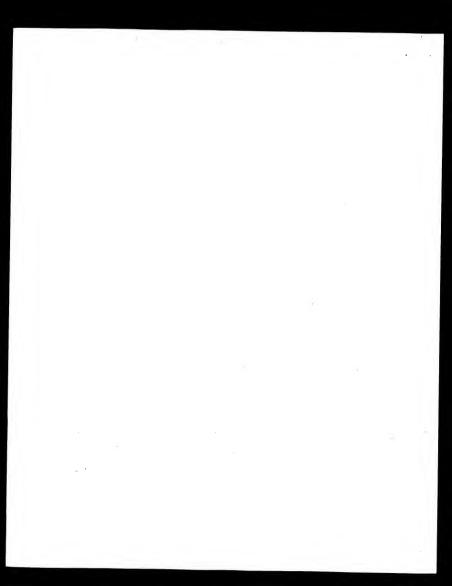
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Query: 689	630	CIDVACSNHGTCITGTCICNPGYKGESCEEVDCMDPTCSGRGVCVRGECHCFVGWGGTNC
1		C CS GTC + C + SC + C P CS C R C + C
Sbjct:	5	CGFPTCSTLGTCGSSCCQPPSCCQPSCCQPVCSQTTCC-RPTCFQSSCCRPSCC
Query:	690	${\tt BTPRATCLDQCSGHGTFLPDTGLCSCDPSWTGHDCSIBICAADCGGHGVCVGGTCRCB}$
Sbjet: 93	58	+T + TC S G+ SC W DC +E GTSCCQPTCCQSSSCQTGCGIGSCRTRWCRPDCRVB
Query:	748	DGWMGAACDQRACHPRCAEHGTCRDGKCECSPGWMGBHC 786 C C C C+ + S F + G+ C
Sbjct:	94	GTCLPPCCVVSCTPPTCCQPVSAQASCCRPSYCGQSC 130

The novel TEN-M-like protein encoded by the gene of invention has highest homology to the mouse TEN-M4 protein, which belongs to the ODZ/TENM family of proteins. This family was first identified in Drosophila as being a pair-rule gene affecting segmentation of the early embryo. It was the first pair-rule gene identified that was not a transcription factor. but a type II transmembrane protein. Vertebrate homologs of the TENM family have been identified in mouse and zebrafish. In the mouse, TEN-M4 expression was found to be on the cell surface, in the brain, trachea as well as developing limb and bone. Analysis of the TEN-M1 protein reveals that it can bind to itself, making it likely that TEN-M4 may be a dimeric moiety as well. In cell culture experiments, fragments of the TEN-M proteins can bind the Drosophila PS2 integrins. In addition, members of the TEN-M family have been identified to be downstream of the endoplasmic reticulum stress response pathway, which alters the response of cells to their environment. This suggests that the ODZ/TENM family may be involved in cell adhesion, spreading and motility. Translocations leading to the fusion of this gene with the NRG1/HGL gene from chromosome 8 have been found to generate a paracrine growth factor for one mammary carcinoma cell line, termed gamma-heregulin. Therefore this novel gene may have widespread implications in development, regeneration and carcinogenesis of various tissues.



Two new potential ligands of the Drosophila PS2 integrins have been characterized by functional interaction in cell culture. These potential ligands are a new Drosophila laminin alpha2 chain encoded by the wing blister locus and Ten-m, an extracellular protein known to be involved in embryonic pattern formation. As with previously identified PS2 ligands, both contain RGD sequences, and RGD-containing fragments of these two proteins (DLAM-RGD and TENM-RGD) can support PS2 integrin-mediated cell spreading. In all cases, this spreading is inhibited specifically by short RGD-containing peptides. As previously found for the PS2 ligand tiggrin (and the tiggrin fragment TIG-RGD), TENM-RGD induces maximal spreading of cells expressing integrin containing the alphaPS2C splice variant. This is in contrast to DLAM-RGD, which is the first Drosophila polypeptide shown to interact preferentially with cells expressing the alphaPS2 m8 splice variant. The betaPS integrin subunit also varies in the presumed ligand binding region as a result of alternative splicing. For TIG-RGD and TENM-RGD, the beta splice variant has little effect, but for DLAM-RGD, maximal cell spreading is supported only by the betaPS4A form of the protein. Thus, the diversity in PS2 integrins due to splicing variations, in combination with diversity of matrix ligands, can greatly enhance the functional complexity of PS2-ligand interactions in the developing animal. The data also suggest that the splice variants may alter regions of the subunits that are directly involved in ligand interactions, and this is discussed with respect to models of integrin structure.

A sequence of about thirty to forty amino-acid residues long found in the sequence of epidermal growth factor (EGF) has been shown to be present, in a more or less conserved form, in a large number of other, mostly animal proteins. The list of proteins currently known to contain one or more copies of an EGF-like pattern is large and varied. The functional significance of EGF domains in what appear to be unrelated proteins is not yet clear. However, a common feature is that these repeats are found in the extracellular domain of membrane-bound proteins or in proteins known to be secreted (exception: prostaglandin G/H synthase). The EGF domain includes six cysteine residues which have been shown (in EGF) to be involved in disulfide bonds. The main structure is a two-stranded beta-sheet followed by a loop to a C-terminal short two-stranded sheet. Subdomains between the conserved cysteines vary in length. The NHL (NCL-1, HT2A and LIN-41) repeat is found in a variety of enzymes of the copper type II, ascorbate-dependent monooxygenase family which catalyse the C-terminus alpha-amidation of biological peptides. The repeat also occurs in a human zinc finger protein that specifically interacts with the activation domain of lentiviral Tat proteins. The repeat domain that is often associated with RING finger and B-box motifs (see, Ben-Zur T,



Dev Biol 2000 Jan 1;217(1):107-20; Adelaide J, Int J Oncol 2000 Apr;16(4):683-8; Wang XZ, Oncogene 1999 Oct 7;18(41):5718-21; Schaefer G, Oncogene 1997 Sep 18;15(12):1385-94; Wang XZ, EMBO J 1998 Jul 1;17(13):3619-30; Baumgartner S, EMBO J 1994 Aug 15;13(16):3728-40; Otaki JM, Dev Biol 1999 Aug 1;212(1):165-81; Mieda M, Mech Dev 1999 Sep;87(1-2):223-7; Oohashi T, J Cell Biol 1999 May 3;145(3):563-77; Graner MW, J Biol Chem 1998 Jul 17;273(29):18235-41, incorporated herein by reference).

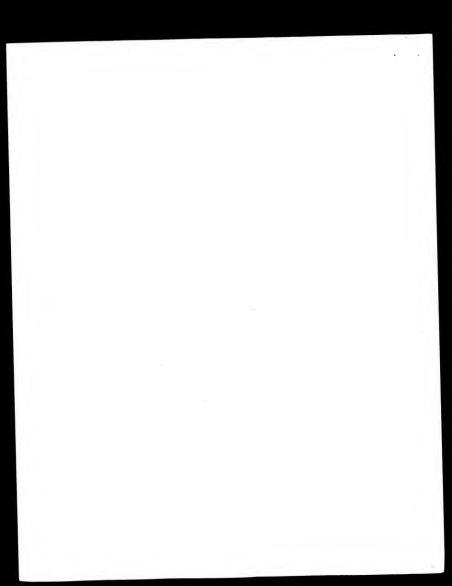
The protein similarity information, expression pattern, and map location for the TEN-M4-like protein and nucleic acid disclosed herein suggest that this TEN-M4-like protein may have important structural and/or physiological functions characteristic of this family.

Therefore, the nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications and as a research tool. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed, as well as potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), and (v) a composition promoting tissue regeneration in vitro and in vivo (vi) biological defense weapon.

The NOV4 nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For example, the compositions of the present invention will have efficacy for treatment of patients suffering from: cardiac diseases, myocardial contractility in failing heart and other diseases, disorders and conditions of the like. The disclosed NOV4 nucleic acid of the invention encoding a TEN-M4-like protein includes the nucleic acid whose sequence is provided in Table 4A or a fragment thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in Table 4A while still encoding a protein that maintains TEN-M4-like protein-like activities and physiological functions, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are complementary to any of the nucleic acids just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be

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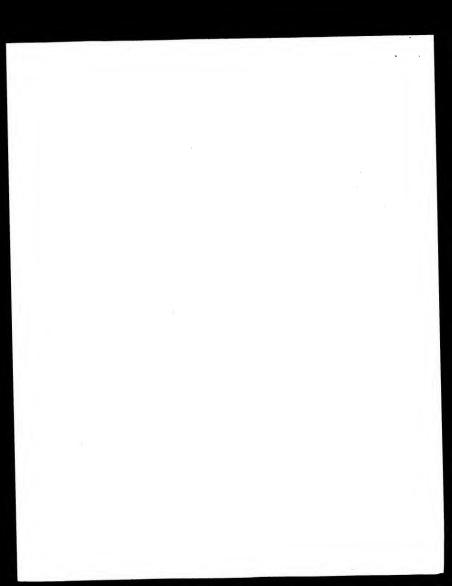
used, for example, as antisense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to about 11 percent of the bases may be so changed.

The disclosed NOV4 protein of the invention includes the TEN-M4-like protein whose sequence is provided in Table 3B. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in Table 4B while still encoding a protein that maintains beta adrenergic receptor kinase-like activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to about 3 percent of the residues may be so changed.

The protein similarity information, expression pattern, and map location for TEN-M4like protein and nucleic acid (NOV4) disclosed herein suggest that NOV4 may have important
structural and/or physiological functions characteristic of the TEN-M4 protein family.

Therefore, the NOV4 nucleic acids and proteins of the invention are useful in potential
diagnostic and therapeutic applications. These include serving as a specific or selective
nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount
of the nucleic acid or the protein are to be assessed, as well as potential therapeutic
applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target,
(iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a
nucleic acid useful in gene therapy (gene delivery/gene ablation), and (v) a composition
promoting tissue regeneration in vitro and in vivo.

The NOV4 nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications implicated in various diseases and disorders described below. For example, the compositions of the present invention will have efficacy for treatment of patients suffering from: Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypocalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-telangicetasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neurodegeneration, fertility disorders, hyperparathyroidism, hypoparathyroidism, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation disorders, diabetes, autoimmune disease, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, hypocalcaemia, asthma, emphysema, scleroderma, allergy, ARDS, Hirschsprung's disease,



WHAT IS CLAIMED IS:

 An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

- (a) a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34;
- (b) a variant of a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of the amino acid residues from the amino acid sequence of said mature form;
- (c) an amino acid sequence selected from the group consisting SEQ ID NOS:2, 4,6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34; and
- (d) a variant of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence.
- 2 The polypeptide of claim 1, wherein said polypeptide comprises the amino acid sequence of a naturally-occurring allelic variant of an amino acid sequence selected from the group consisting SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34.
- The polypeptide of claim 2, wherein said allelic variant comprises an amino acid
 sequence that is the translation of a nucleic acid sequence differing by a single
 nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID
 NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, and 35.
- The polypeptide of claim 1, wherein the amino acid sequence of said variant comprises
 a conservative amino acid substitution.

An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a
polypeptide comprising an amino acid sequence selected from the group consisting of:

- (a) a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34;
- (b) a variant of a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of the amino acid residues from the amino acid sequence of said mature form;
- (c) an amino acid sequence selected from the group consisting of SEQ ID NOS:2,4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34;
- (d) a variant of an amino acid sequence selected from the group consisting SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, and 34, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence;
- (e) a nucleic acid fragment encoding at least a portion of a polypeptide comprising an amino acid sequence chosen from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, or a variant of said polypeptide, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence; and
- (f) a nucleic acid molecule comprising the complement of (a), (b), (c), (d) or (e).
- The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises the nucleotide sequence of a naturally-occurring allelic nucleic acid variant.
- The nucleic acid molecule of claim 5, wherein the nucleic acid molecule encodes a
 polypeptide comprising the amino acid sequence of a naturally-occurring polypeptide
 variant.

 The nucleic acid molecule of claim 5, wherein the nucleic acid molecule differs by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, and 35.

- The nucleic acid molecule of claim 5, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:
 - (a) a nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 3,5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, and 35:
 - (b) a nucleotide sequence differing by one or more nucleotides from a nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, and 35, provided that no more than 20% of the nucleotides differ from said nucleotide sequence:
 - (c) a nucleic acid fragment of (a); and
 - (d) a nucleic acid fragment of (b).
- 10. The nucleic acid molecule of claim 5, wherein said nucleic acid molecule hybridizes under stringent conditions to a nucleotide sequence chosen from the group consisting SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, and 35, or a complement of said nucleotide sequence.
- 11. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:
 - (a) a first nucleotide sequence comprising a coding sequence differing by one or more nucleotide sequences from a coding sequence encoding said amino acid sequence, provided that no more than 20% of the nucleotides in the coding sequence in said first nucleotide sequence differ from said coding sequence:
 - an isolated second polynucleotide that is a complement of the first polynucleotide; and
 - (c) a nucleic acid fragment of (a) or (b).
- A vector comprising the nucleic acid molecule of claim 11.
- 13. The vector of claim 12, further comprising a promoter operably-linked to said nucleic acid molecule.

- 14. A cell comprising the vector of claim 12.
- 15. An antibody that binds immunospecifically to the polypeptide of claim 1.
- 16. The antibody of claim 15, wherein said antibody is a monoclonal antibody.
- 17. The antibody of claim 15, wherein the antibody is a humanized antibody.
- 18. A method for determining the presence or amount of the polypeptide of claim 1 in a sample, the method comprising:
 - (a) providing the sample;
 - (b) contacting the sample with an antibody that binds immunospecifically to the polypeptide; and
- (c) determining the presence or amount of antibody bound to said polypeptide, thereby determining the presence or amount of polypeptide in said sample.
- 19. A method for determining the presence or amount of the nucleic acid molecule of claim 5 in a sample, the method comprising:
 - (a) providing the sample;
 - (b) contacting the sample with a probe that binds to said nucleic acid molecule; and
 - (c) determining the presence or amount of the probe bound to said nucleic acid molecule,

thereby determining the presence or amount of the nucleic acid molecule in said sample.

- 20. The method of claim 19 wherein presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.
- 21. The method of claim 20 wherein the cell or tissue type is cancerous.
- 22. A method of identifying an agent that binds to a polypeptide of claim 1, the method comprising:
 - (a) contacting said polypeptide with said agent; and
 - (b) determining whether said agent binds to said polypeptide.

23. The method of claim 22 wherein the agent is a cellular receptor or a downstream effector.

- 24. A method for identifying an agent that modulates the expression or activity of the polypeptide of claim 1, the method comprising:
 - (a) providing a cell expressing said polypeptide:
 - (b) contacting the cell with said agent, and
 - determining whether the agent modulates expression or activity of said polypeptide,

whereby an alteration in expression or activity of said peptide indicates said agent modulates expression or activity of said polypeptide.

- 25. A method for modulating the activity of the polypeptide of claim 1, the method comprising contacting a cell sample expressing the polypeptide of said claim with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptide.
- 26. A method of treating or preventing a NOVX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the polypeptide of claim 1 in an amount sufficient to treat or prevent said NOVX-associated disorder in said subject.
- The method of claim 26 wherein the disorder is selected from the group consisting of cardiomyopathy and atherosclerosis.
- 28. The method of claim 26 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
- The method of claim 26, wherein said subject is a human.
- A method of treating or preventing a NOVX-associated disorder, said method
 comprising administering to a subject in which such treatment or prevention is desired

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the nucleic acid of claim 5 in an amount sufficient to treat or prevent said NOVX-associated disorder in said subject.

- The method of claim 30 wherein the disorder is selected from the group consisting of cardiomyopathy and atherosclerosis.
- The method of claim 30 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
- 33. The method of claim 30, wherein said subject is a human.
- 34. A method of treating or preventing a NOVX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the antibody of claim 15 in an amount sufficient to treat or prevent said NOVX-associated disorder in said subject.
- The method of claim 34 wherein the disorder is diabetes.
- The method of claim 34 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
- The method of claim 34, wherein the subject is a human.
- A pharmaceutical composition comprising the polypeptide of claim 1 and a pharmaceutically-acceptable carrier.
- A pharmaceutical composition comprising the nucleic acid molecule of claim 5 and a pharmaceutically-acceptable carrier.
- A pharmaceutical composition comprising the antibody of claim 15 and a pharmaceutically-acceptable carrier.
- 41. A kit comprising in one or more containers, the pharmaceutical composition of claim

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42. A kit comprising in one or more containers, the pharmaceutical composition of claim

- A kit comprising in one or more containers, the pharmaceutical composition of claim
- 44. A method for determining the presence of or predisposition to a disease associated with altered levels of the polypeptide of claim 1 in a first mammalian subject, the method comprising:
 - measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and
 - comparing the amount of said polypeptide in the sample of step (a) to the amount of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, said disease;

wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to said disease.

- 45. The method of claim 44 wherein the predisposition is to a cancer.
- 46. A method for determining the presence of or predisposition to a disease associated with altered levels of the nucleic acid molecule of claim 5 in a first mammalian subject, the method comprising:
 - measuring the amount of the nucleic acid in a sample from the first mammalian subject; and
- (b) comparing the amount of said nucleic acid in the sample of step (a) to the amount of the nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease; wherein an alteration in the level of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.
- The method of claim 46 wherein the predisposition is to a cancer.

48. A method of treating a pathological state in a mammal, the method comprising administering to the mammal a polypeptide in an amount that is sufficient to alleviate the pathological state, wherein the polypeptide is a polypeptide having an amino acid sequence at least 95% identical to a polypeptide comprising an amino acid sequence of at least one of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, and 34, or a biologically active fragment thereof.

49. A method of treating a pathological state in a mammal, the method comprising administering to the mammal the antibody of claim 15 in an amount sufficient to alleviate the pathological state.